FIG. 1

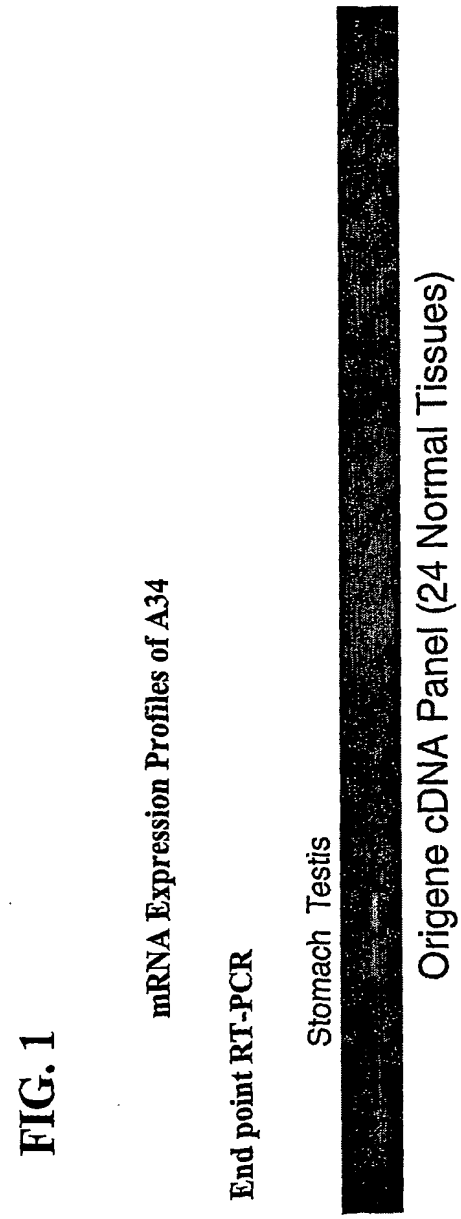

mRNA Expression Profiles of A34
End point RT-PCR
Stomach Testis
Origene cDNA Panel (24 Normal Tissues)

FIG. 2

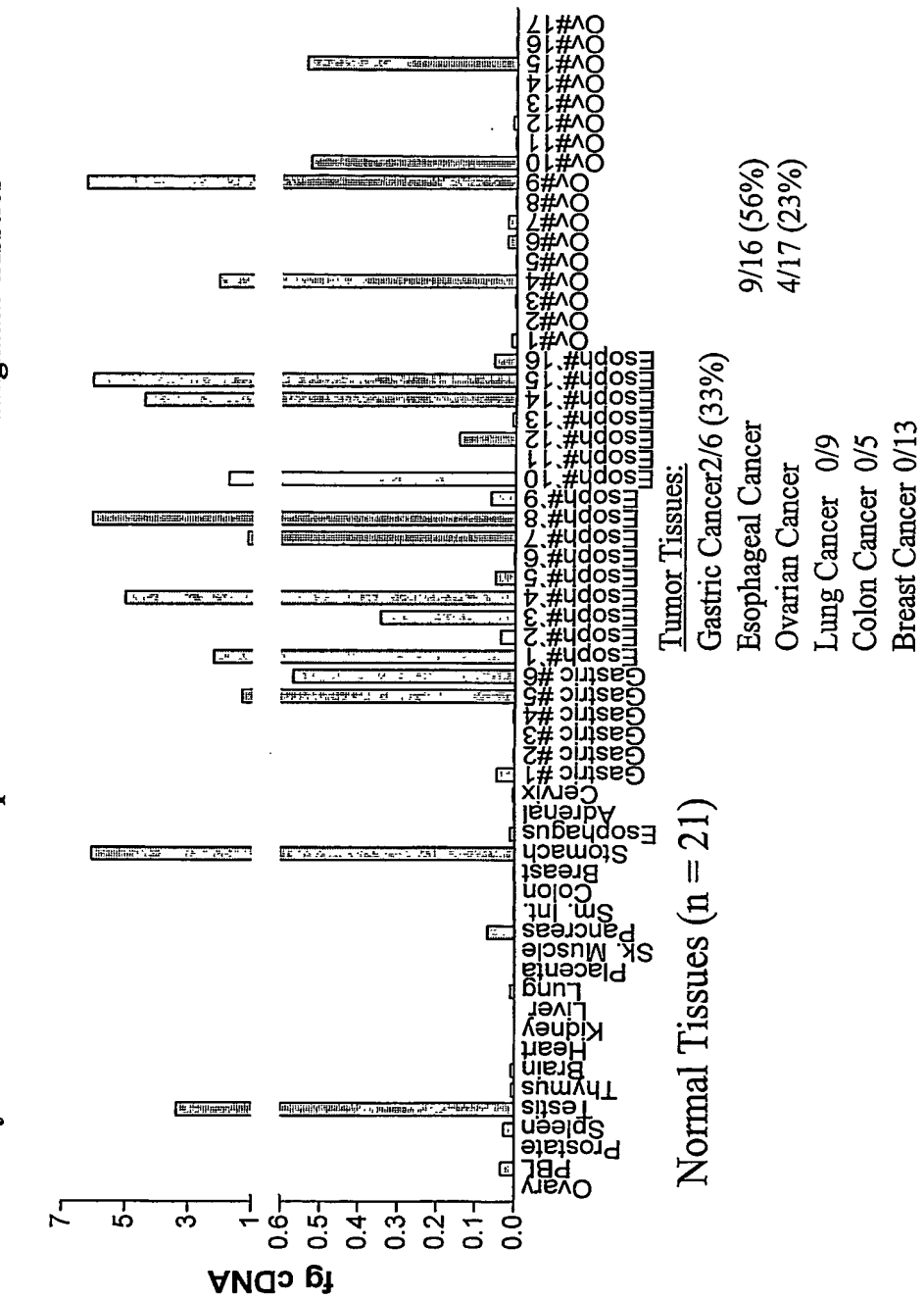
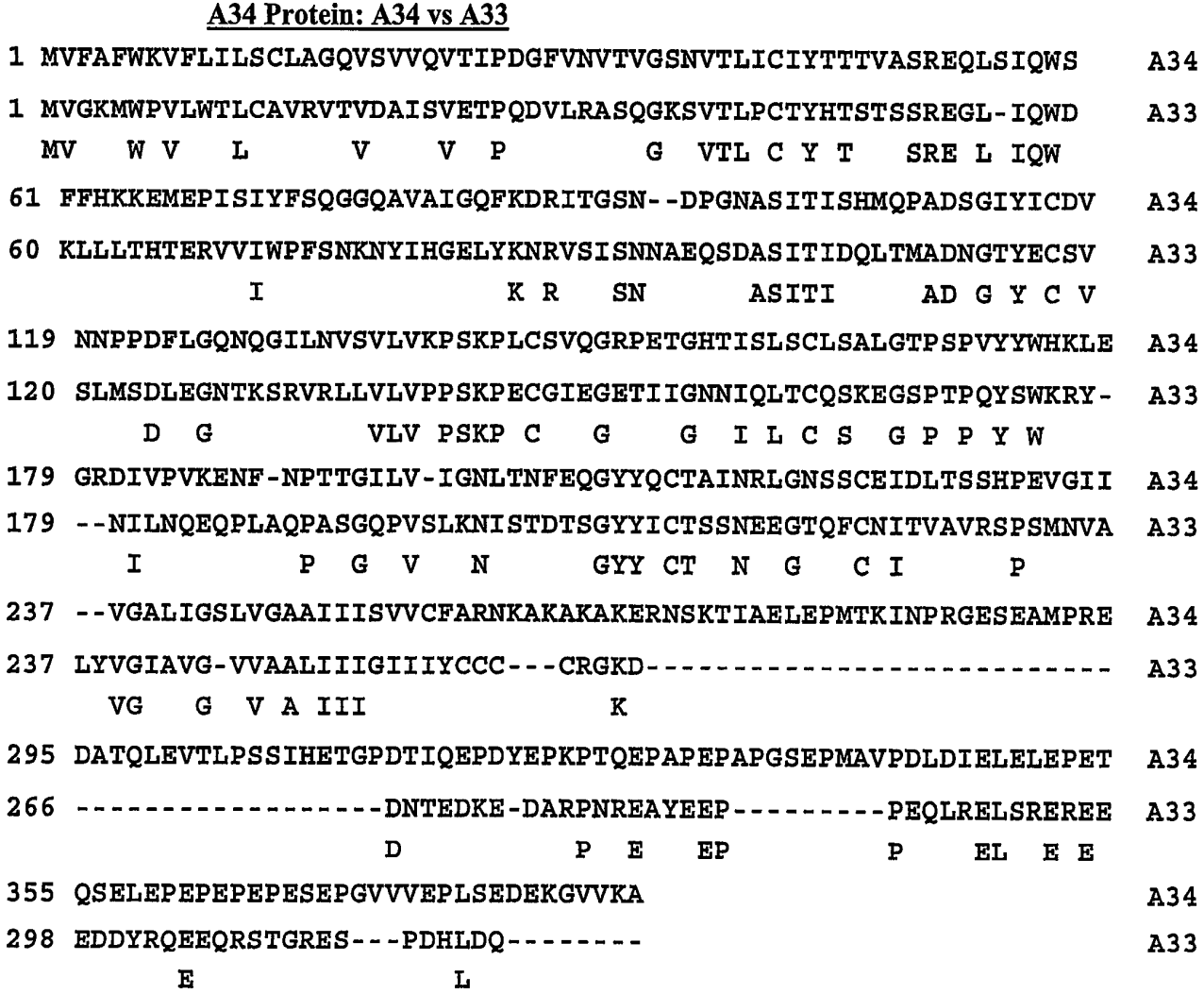

Analysis of A34 mRNA Expression in Normal and Malignant Tissues
fg cDNA
7
5
3
1
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Normal Tissues (n = 21)
Ovary
PBL
Prostate
Spleen
Testis
Thymus
Brain
Heart
Kidney
Liver
Lung
Placenta
Sk. Muscle
Pancreas
Sm. Int.
Colon
Breast
Stomach
Esophagus
Adrenal
Cervix
Gastric #1
Gastric #2
Gastric #3
Gastric #4
Gastric #5
Gastric #6
Tumor Tissues:
Gastric Cancer2/6 (33%)
Esophageal Cancer 9/16 (56%)
Ovarian Cancer 4/17 (23%)
Lung Cancer 0/9
Colon Cancer 0/5
Breast Cancer 0/13

FIG. 3


A34 Protein: A34 vs A33
1 MVFAFWKVFLILSCLAGQVSVVQVTIPDGFVNVTVGSNVTLICIYTTTVASREQLSIQWS A34
1 MVGKMWPVLWTLCAVRVTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGL-IQWD A33
MV W V L V V P G VTL C Y T SRE L IQW
61 FFHKKEMEPISIYFSQGGQAVAIGQFKDRITGSN--DPGNASITISHMQPADSGIYICDV A34
60 KLLLTHTERVVIWPFSNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSV A33
I K R SN ASITI AD G Y C V
119 NNPPDFLGQNQGILNVSVLVKPSKPLCSVQGRPETGHTISLSCLSALGTPSPVYYWHKLE A34
120 SLMSDLEGNTKSRVRLLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRY- A33
D G VLV PSKP C G G I L C S G P P Y W
179 GRDIVPVKENF-NPTTGILV-IGNLTNFEQGYYQCTAINRLGNSSCEIDLTSSHPEVGII A34
179 --NILNQEQPLAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVA A33
I P G V N GYY CT N G C I P
237 --VGALIGSLVGAAIIISVVCFARNKAKAKAKERNSKTIAELEPMTKINPRGESEAMPRE A34
237 LYVGIAVG-VVAALIIIGIIIYCCC---CRGKD---------- A33
VG G V A III K
295 DATQLEVTLPSSIHETGPDTIQEPDYEPKPTQEPAPEPAPGSEPMAVPDLDIELELEPET A34
266 ----------DNTEDKE-DARPNREAYEEP---------PEQLRELSREREE A33
D P E EP P EL E E
355 QSELEPEPEPEPESEPGVVVEPLSEDEKGVVKA A34
298 EDDYRQEEQRSTGRES---PDHLDQ-------- A33
E L

A34: Nucleic acid sequence (SEQ ID NO: 3):

CTTCTTGTGGTAGGGACCTCTCCTCAGTATTTGAAACTAACCAGCATCTGACAGA
TTTCGAATTTGTAAAAAATACCCTCGAAGATTCAGGAATGAAGCTTCTGTGTGAA
GGATTAAAACAGCCCAACTGTGTATTACAGACATTGAGGTGGTACCGGTGCCTTA
TCTCTTCTGCTTCTTGTGGGGCTCTAGCAGCTGTTCTTAGCACCAGTCAGTGGCT
CACTGAACTGGAATTTAGTGAGACAAAACTGGAAGCTTCAGCTTTGAAATTGCTC
TATGGAGGCTTAAAAGATCCAAATTGCAAATTACAGAAGCTCAACTTGCAGTTTT
CTTTATCTGTAACCGCTGCAAAACTTCCAGTTGGAATGGTTGGAAATTGTTCTGG
TTTCTCGGGATCATTGGTGCAATCTCATTTTGGCTACTGTCAGGACAGTTCTTTC
AAATGTGATCTTTGTAAGCTGCTCTGGCCTTCCACCAGAGTTGCTGCTGCAAAGG
ATTGTGGGAGTCCTAAGTCCTTCCTATCAGAAGGGCTGAACTGGGCAGGAAGACT
TGAGGCAGTGGAGGAGGTTTTGGGGTTGGGGGTGCTTGTACAGCCCGGTGACCCA
GCATCTCAGGGTGGGGGGCATTGTGAAAACTATGGGTCTTTTAGAGACTTGGTGG
ACTTAGAAGTCAAGGCAGAACCAAGCCTGAGAAAAGGTGGTATGGATCTCCAGAG
ACCCACCCTACAAGTTGTCCTCCTTTGCAAAATCTTCTCCCTCAAACTATTTCTC
TTTATTGCATTGCCTAATTCTCCTGGTCAGGTTAGTGTGGTGCAAGTGACCATCC
CAGACGGTTTCGTGAACGTGACTGTTGGATCTAATGTCACTCTCATCTGCATCTA
CACCACCACTGTGGCCTCCCGAGAACAGCTTTCCATCCAGTGGTCTTTCTTCCAT
AAGAAGGAGATGGAGCCAATTTCTATTTACTTTTCTCAAGGTGGACAAGCTGTAG
CCATCGGGCAATTTAAAGATCGAATTACAGGGTCCAACGATCCAGGTAATGCATC
TATCACTATCTCGCATATGCAGCCAGCAGACAGTGGAATTTACATCTGCGATGTT
AACAACCCCCCAGACTTTCTCGGCCAAAACCAAGGCATCCTCAACGTCAGTGTGT
TAGTGAAACCTTCTAAGCCCCTTTGTAGCGTTCAAGGAAGACCAGAAACTGGCCA
CACTATTTCCCTTTCCTGTCTCTCTGCGCTTGGAACACCTTCCCCTGTGTACTAC
TGGCATAAACTTGAGGGAAGAGACATCGTGCCAGTGAAAGAAAACTTCAACCCAA
CCACCGGGATTTTGGTCATTGGAAATCTGACAAATTTTGAACAAGGTTATTACCA
GTGTACTGCCATCAACAGACTTGGCAATAGTTCCTGCGAAATCGATCTCACTTCT
TCACATCCAGAAGTTGGAATCATTGTTGGGGCCTTGATTGGTAGCCTGGTAGGTG
CCGCCATCATCATCTCTGTTGTGTGCTTCGCAAGGAATAAGGCAAAAGCAAAGGC
AAAAGAAAGAAATTCTAAGACCATCGCGGAACTTGAGCCAATGACAAAGATAAAC
CCAAGGGGAGAAAGCGAAGCAATGCCAAGAGAAGACGCTACCCAACTAGAAGTAA
CTCTACCATCTTCCATTCATGAGACTGGCCCTGATACCATCCAAGAACCAGACTA
TGAGCCAAAGCCTACTCAGGAGCCTGCCCCAGAGCCTGCCCCAGGATCAGAGCCT
ATGGCAGTGCCTGACCTTGACATCGAGCTGGAGCTGGAGCCAGAAACGCAGTCGG
AATTGGAGCCAGAGCCAGAGCCAGAGCCAGAGTCAGAGCCTGGGGTTGTAGTTGA
GCCCTTAAGTGAAGATGAAAAGGGAGTGGTTAAGGCATAG

A34 amino acid sequence (SEQ ID NO: 4):

MDLQRPTLQVVLLCKIFSLKLFLFIALPNSPGQVSVVQVTIPDGFVNVTVGSNVT
LICIYTTTVASREQLSIQWSFFHKKEMEPISIYFSQGGQAVAIGQFKDRITGSND
PGNASITISHMQPADSGIYICDVNNPPDFLGQNQGILNVSVLVKPSKPLCSVQGR
PETGHTISLSCLSALGTPSPVYYWHKLEGRDIVPVKENFNPTTGILVIGNLTNFE
QGYYQCTAINRLGNSSCEIDLTSSHPEVGIIVGALIGSLVGAAIIISVVCFARNK
AKAKAKERNSKTIAELEPMTKINPRGESEAMPREDATQLEVTLPSSIHETGPDTI
QEPDYEPKPTQEPAPEPAPGSEPMAVPDLDIELELEPETQSELEPEPEPEPESEP
GVVVEPLSEDEKGVVKA

FIG. 4

A34 clone nucleic acid sequence (SEQ. ID NO: 5)

ACTGTTGGATCTAATGTCACTCTCATCTGCATCTACACCACCACTGTGGCCTCCCGAGA
ACAGCTTTCCATCCAGTGGTCTTTCTTCCATAAGAAGGAGATGGAGCCAATTTCTATTT
ACTTTTCTCAAGGTGGACAAGCTGTAGCCATCGGGCAATTTAAAGATCGAATTACAGGG
TCCAACGATCCAGGTAATGCATCTATCACTATCTCGCATATGCAGCCAGCAGACAGTGG
AATTTACATCTGCGATGTTAACAACCCCCCAGACTTTCTCGGCCAAAACCAAGGCATCC
TCAACGTCAGTGTGTTAGTGAAACCTTCTAAGCCCCTTTGTAGCGTTCAAGGAAGACCA
GAAACTGGCCACACTATTTCCCTTTCCTGTCTCTCTGCGCTTGGAACACCTTCCCCTGT
GTACTACTGGCATAAACTTGAGGGAAGAGACATCGTGCCAGTGAAAGAAAACTTCAACC
CAACCACCGGGATTTTGGTCATTGGAAATCTGACAAATTTTGAACAAGGTTATTACCAG
TGTACTGCCATCAACAGACTTGGCAATAGTTCCTGCGAAATCGATCTCACTTCTTCACA
TCCAGAAGTTGGAATCATTGTTGGGGCCTTGATTGGTAGCCTGGTAGGTGCCGCCATCA
TCATCTCTGTTGTGTGCTTCGCAAGGAATAAGGCAAAAGCAAAGGCAAAAGAAAGAAAT
TCTAAGACCATCGCGGAACTTGAGCCAATGACAAAGATAAACCCAAGGGGAGAAAGCGA
AGCAATGCCAAGAGAAGACGCTACCCAACTAGAAGTAACTCTACCATCTTCCATTCATG
AGACTGGCCCTGATACCATCCAAGAACCAGACTATGAGCCAAAGCCTACTCAGGAGCCT
GCCCCAGAGCCTGCCCCAGGATCAGAGCCTATGGCAGTGCCTGACCTTGACATCGAGCT
GGAGCTGGAGCCAGAAACGCAGTCGGAATTGGAGCCAGAGCCAGAGCCAGAGCCAGAGT
CAGAGCCTGGGGTTGTAGTTGAGCCCTTAAGTGAAGATGAAA

A34 clone amino acid sequence (SEQ. ID NO: 6)

TVGSNVTLICIYTTTVASREQLSIQWSFFHKKEMEPISIYFSQGGQAVAIGQFKDRITG
SNDPGNASITISHMQPADSGIYICDVNNPPDFLGQNQGILNVSVLVKPSKPLCSVQGRP
ETGHTISLSCLSALGTPSPVYYWHKLEGRDIVPVKENFNPTTGILVIGNLTNFEQGYYQ
CTAINRLGNSSCEIDLTSSHPEVGIIVGALIGSLVGAAIIISVVCFARNKAKAKAKERN
SKTIAELEPMTKINPRGESEAMPREDATQLEVTLPSSIHETGPDTIQEPDYEPKPTQEP
APEPAPGSEPMAVPDLDIELELEPETQSELEPEPEPEPESEPGVVVEPLSEDE

FIGURE 5

A33-like 3 polynucleotide sequence (SEQ ID NO: 7):

TGTGCAGGCAACAGGAAACAAATACAGAGGGCAGAGCAAGGATTGGTCAGGACGG
GCTTAGTGAGAAAGGCTCTGAACGAGACACACACCAGCTGCAGCTTCGTACTGAC
GCCTGCCAGCTCCTACACACCTTCCTGGGCAACTGCCAGCGGGGCAAGGCAGGCC
TGGGGCCACCCTGCAGGCAGTGTCTGGGCCCTCAGCTCCCCCTCCCTCCACCTAC
CCCCTCACACCCACCACTACGACCCCACGGGATACCCAGCCCAGACGGAGGAAAC
ACCGAGCCTAGAGACATGAGAGTTGGAGGAGCATTCCACCTTCTACTCGTGTGCC
TGAGCCCAGCACTGCTGTCTGCTGTGCGGATCAACGGGGATGGACAGGAGGTCCT
GTACCTGGCAGAAGGTGATAATGTGAGGCTGGGCTGCCCCTACGTCCTGGACCCT
GAGGACTATGGTCCCAATGGGCTGGACATCGAGTGGATGCAGGTCAACTCAGACC
CCGCCCACCACCGAGAGAACGTGTTCCTTAGTTACCAGGACAAGAGGATCAACCA
TGGCAGCCTTCCCCATCTGCAGCAGAGGGTCCGCTTTGCAGCCTCAGACCCAAGC
CAGTACGATGCCTCCATCAACCTCATGAACCTGCAGGTATCTGATACAGCCACTT
ATGAGTGCCGGGTGAAGAAGACCACCATGGCCACCCGGAAGGTCATTGTCACTGT
CCAAGCACGACCTGCAGTGCCCATGTGCTGGACAGAGGGCCACATGACATATGGC
AACGATGTGGTGCTGAAGTGCTATGCCAGTGGGGGCTCCCAGCCCCTCTCCTACA
AGTGGGCCAAGATCAGTGGGCACCATTACCCCTATCGAGCTGGGTCTTACACCTC
CCAGCACAGCTACCACTCAGAGCTGTCCTACCAGGAGTCCTTCCACAGCTCCATA
AACCAAGGCCTGAACAATGGGGACCTGGTGTTGAAGGATATCTCCAGAGCAGATG
ATGGGCTGTATCAGTGCACAGTGGCCAACAACGTGGGCTACAGTGTTTGTGTGGT
GGAGGTGAAGGTCTCAGACTCCCGGCGTATAGGCGTGATCATCGGCATCGTCCTG
GGCTCTCTGCTCGCGCTGGGCTGCCTGGCCAGAGGACGCCGTGGCGCCCGGGTGC
AAGGCCAGCGGGCGCGGCAGCCGCGTCACCCACCTCCTGGGGTACCCGACGCAGA
ACGTCAGCCGCTCCCTGCGCCGCAATACGCGCCTCCCCCCTGCGGCGGCCCCGAG
GACGTGGCCCTGGCGCCCTGCACCGCCGCCGCCGCCTGCGAAGCGGGCCCCTCCC
CGGTCTACGTCAAGGTCAAGAGCGCGGAGCCGGCTGACTGCGCCGAGGGGCCGGT
GCAGTGCAAGAACGGCCTCTTGGTGTGA

A33-like 3 polypeptide sequence (SEQ ID NO: 8):

MRVGGAFHLLLVCLSPALLSAVRINGDGQEVLYLAEGDNVRLGCPYVLDPEDYGP
NGLDIEWMQVNSDPAHHRENVFLSYQDKRINHGSLPHLQQRVRFAASDPSQYDAS
INLMNLQVSDTATYECRVKKTTMATRKVIVTVQARPAVPMCWTEGHMTYGNDVVL
KCYASGGSQPLSYKWAKISGHHYPYRAGSYTSQHSYHSELSYQESFHSSINQGLN
NGDLVLKDISRADDGLYQCTVANNVGYSVCVVEVKVSDSRRIGVIIGIVLGSLLA
LGCLARGRRGARVQGQRARQPRHPPPGVPDAERQPLPAPQYAPPPCGGPEDVALA
PCTAAAACEAGPSPVYVKVKSAEPADCAEGPVQCKNGLLV

FIG. 6

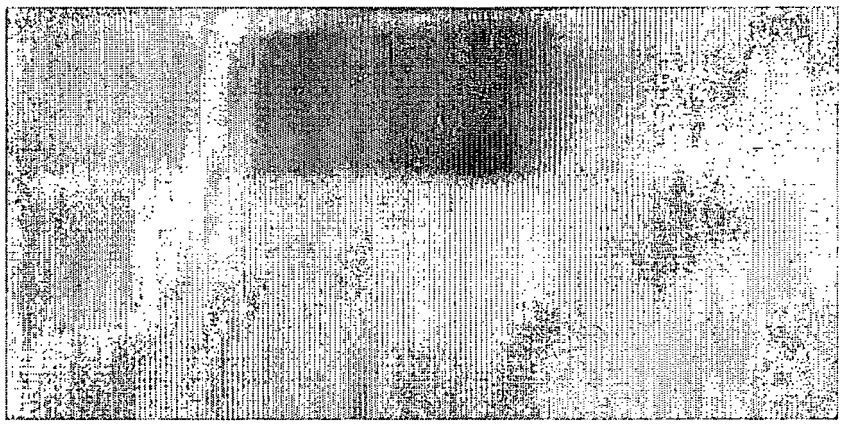
A33-like 3 vs A33:

Score = 67.4 bits (163), Expect = 2e-10
Identities = 63/232 (27%), Positives = 95/232 (40%), Gaps = 35/232 (15%)

```
Query: 29  QEVLYLAEGDNVRLGCPYVLDPEDYGPNGLDIEWMQVNSDPAHHRENVFLSYQDKRINHG 88
           Q+VL  ++G +V L C Y          GL I+W ++     H    V   + +K   HG
A33  : 28  QDVLRASQGKSVTLPCTYHTSTSSR--EGL-IQWDKLLL--THTERVVIWPFSNKNYIHG 82

Query: 89  SLPHLQQRVRFAASDPSQYDASINLMNLQVSDTATYECRVKKTT----MATRKVIVTVQA 144
            L   + RV  + ++  Q DASI +  L ++D  TYEC V   +         +V + V
A33  : 83  EL--YKNRVSIS-NNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLLVLV 139

Query: 145 RPAVPMCWTEGHMTYGNDVVLKCYASGGSQPLSYKWAKISGHHYPYRAGSYTSQHSYHSE 204
            P+ P C  EG    GN++ L C +  GS    Y W + +
A33  : 140 PPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYN-------------------- 179

Query: 205 LSYQESFHSSINQGLNNGDLVLKDISRADDGLYQCTVANNVGYSVCVVEVKV 256 (SEQ. ID NO: 9)
           +  QE     + Q  +   + LK+IS    G Y CT +N  G   C + V V
A33  : 180 ILNQE---QPLAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAV 228 (SEQ. ID NO: 10)
```

FIG. 7

FIG. 8


Normal Colonic Mucosa
Normal Gastric Mucosa
A34 Western Blot with mAb 342
- 55 kDa

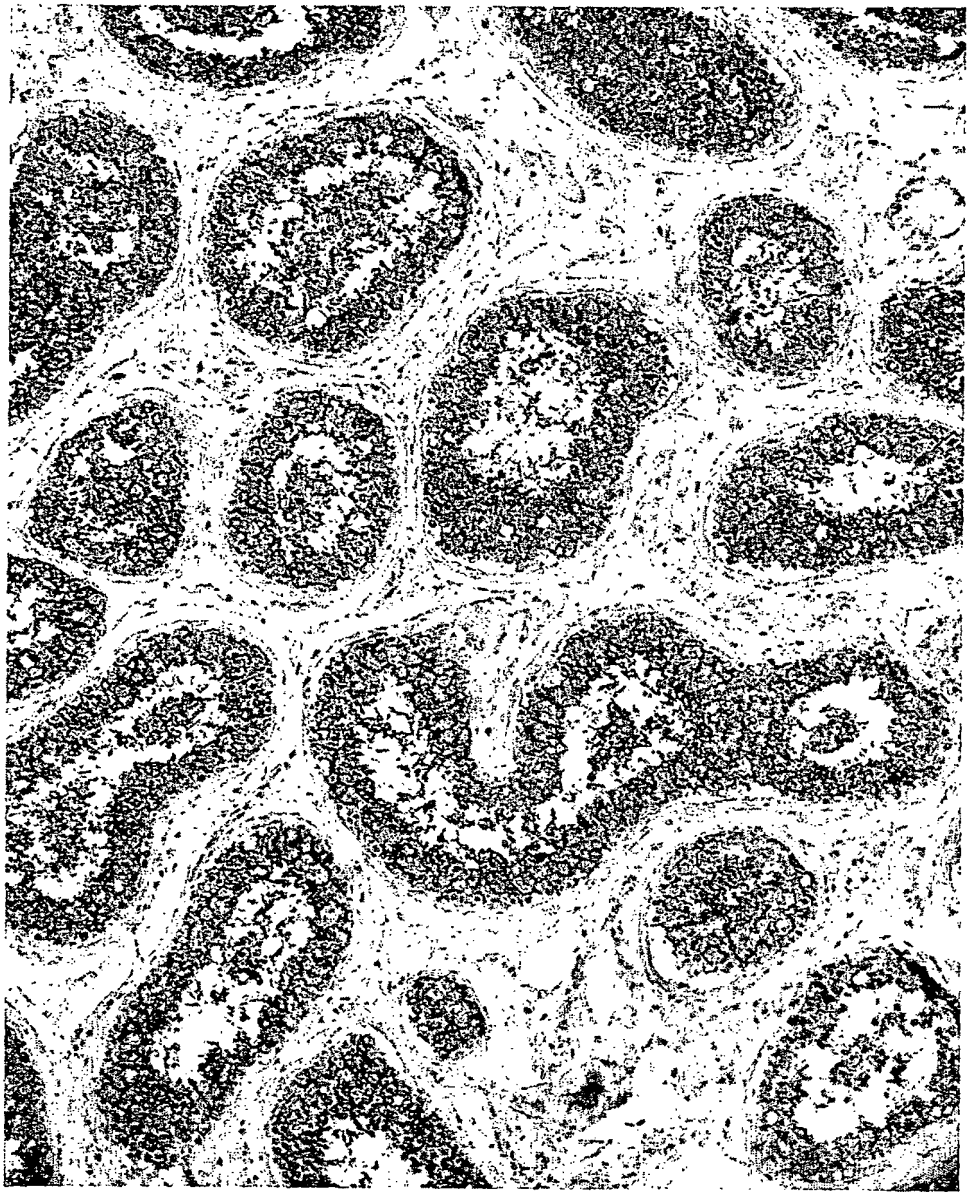


FIG. 9

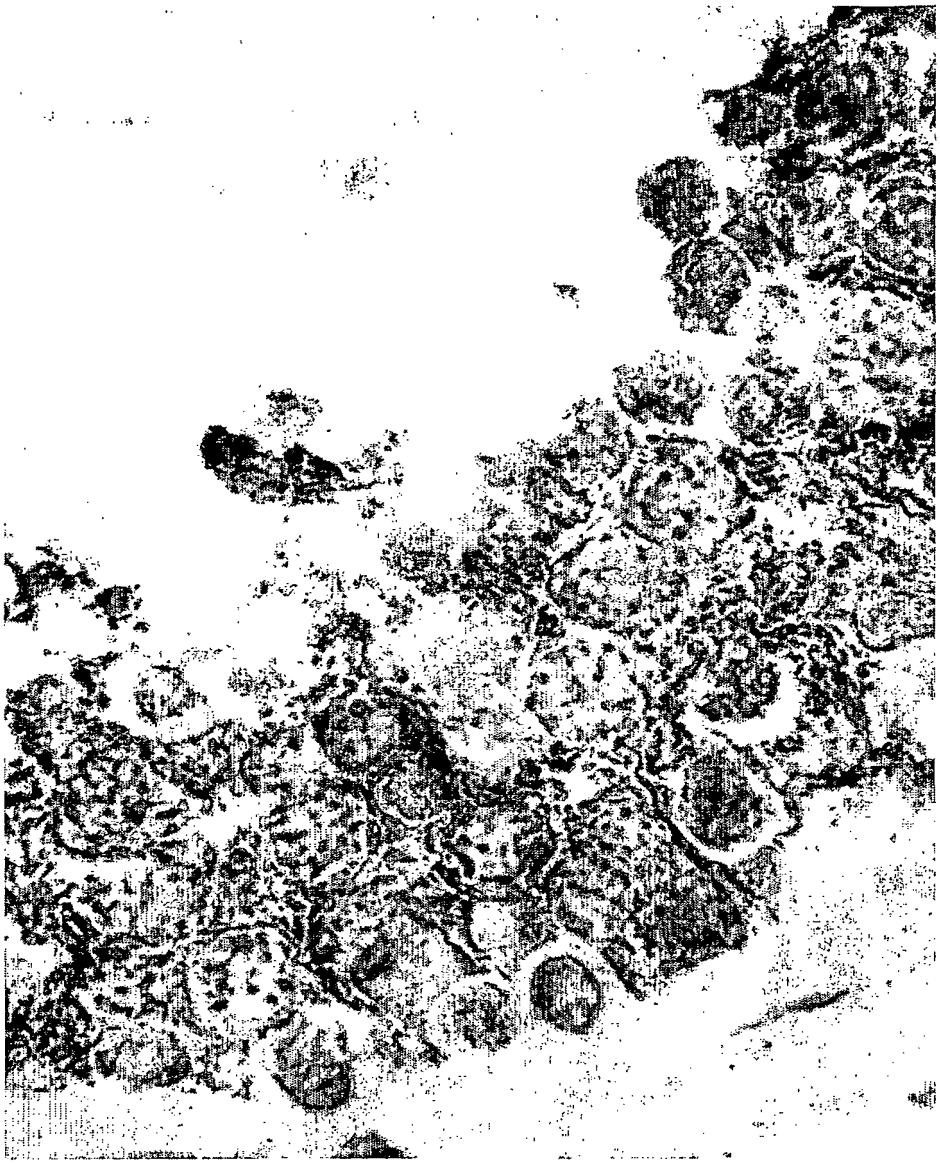


FIG. 10

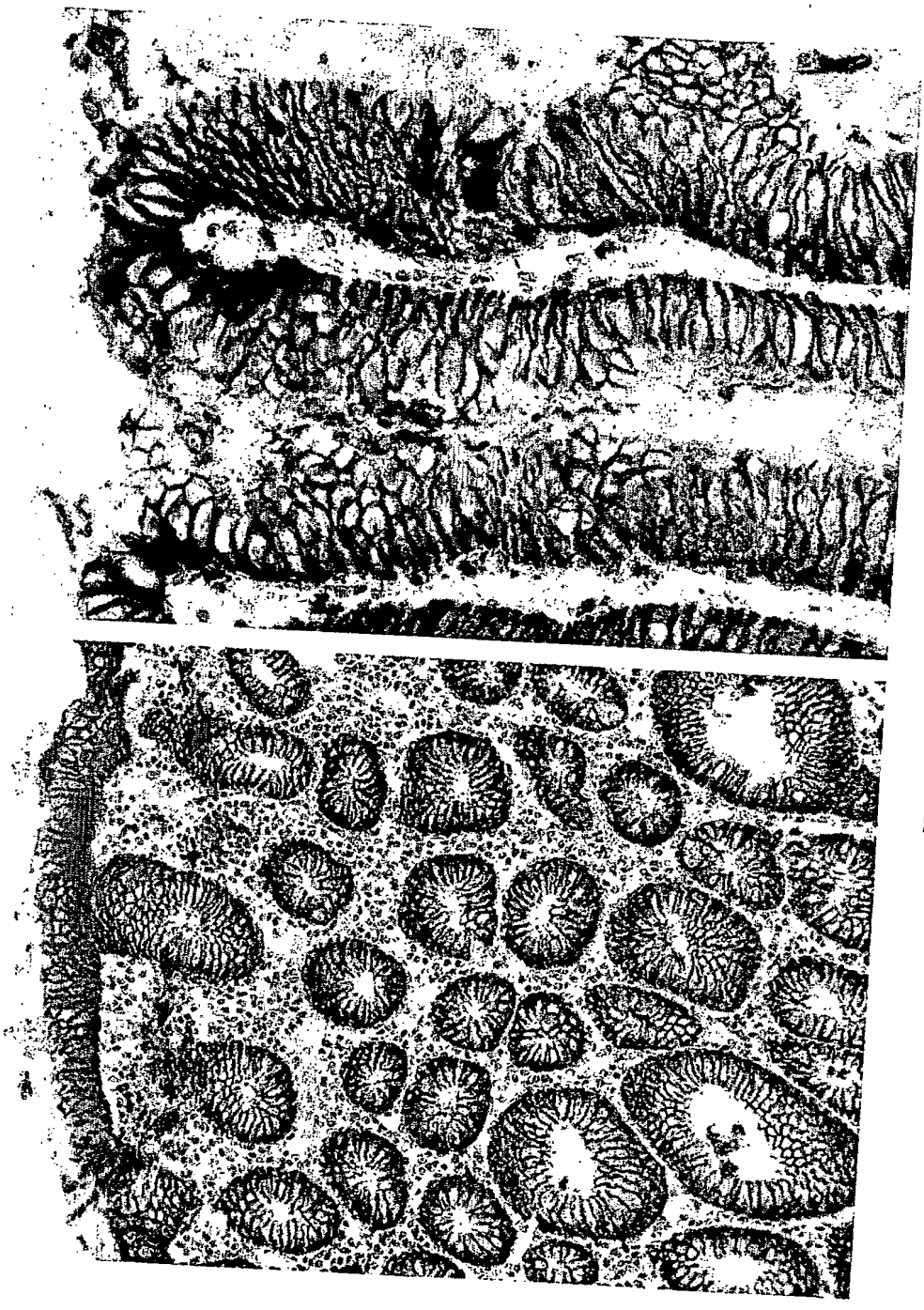


FIG. 11

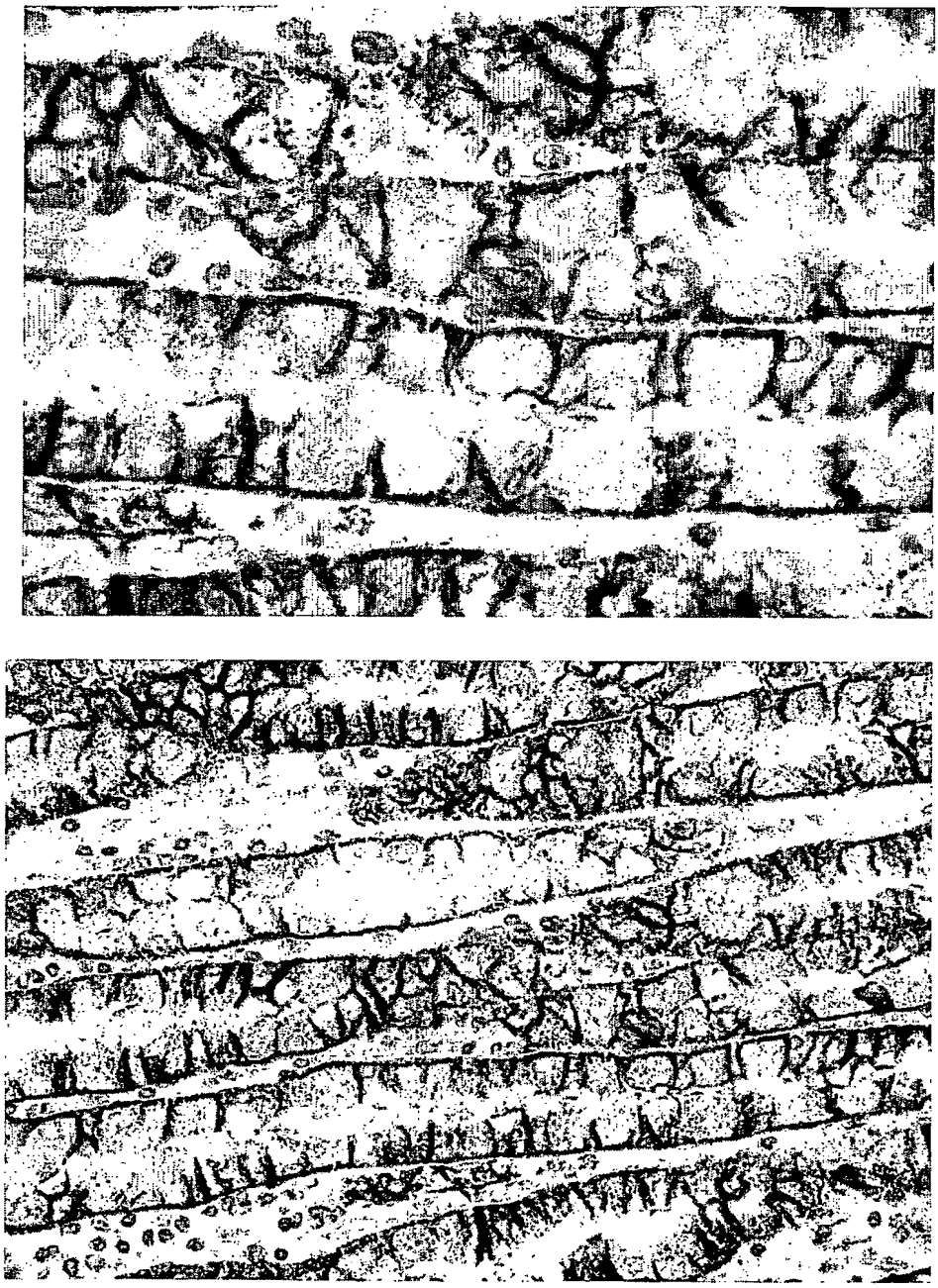


FIG. 12

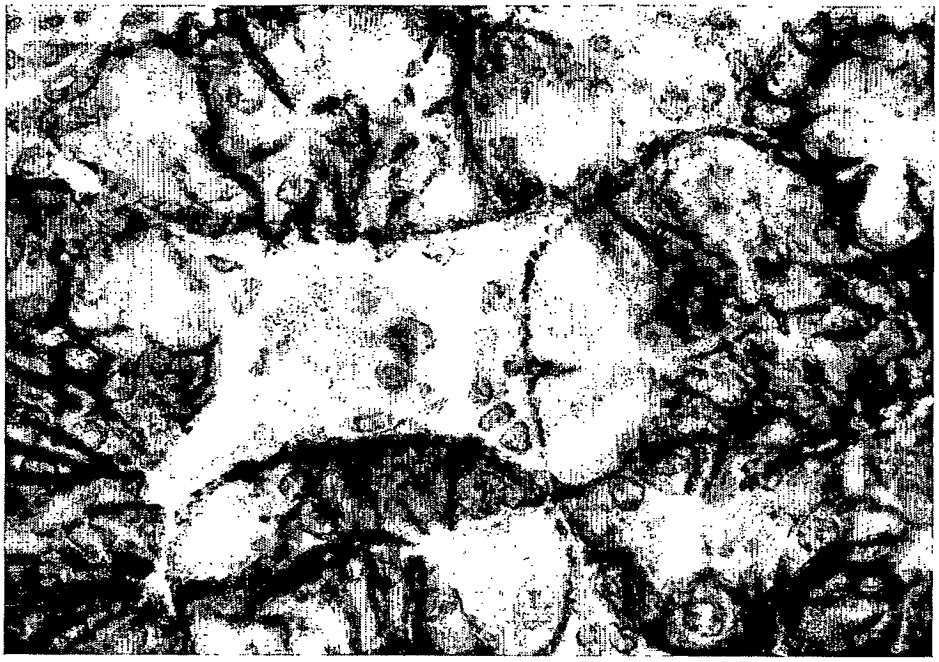


FIG. 14

FIG. 13

FIG. 16

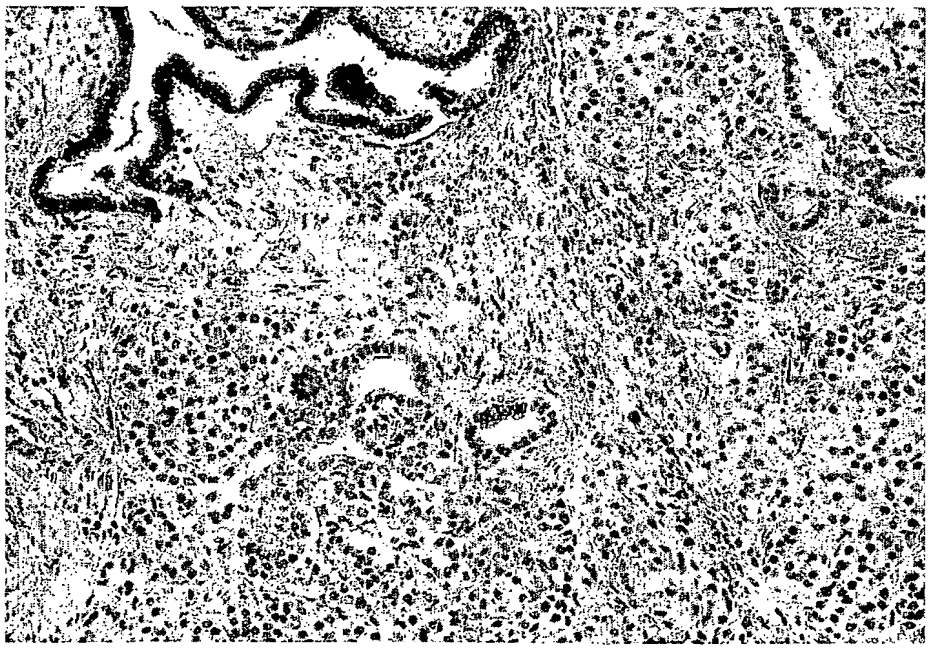


FIG. 15

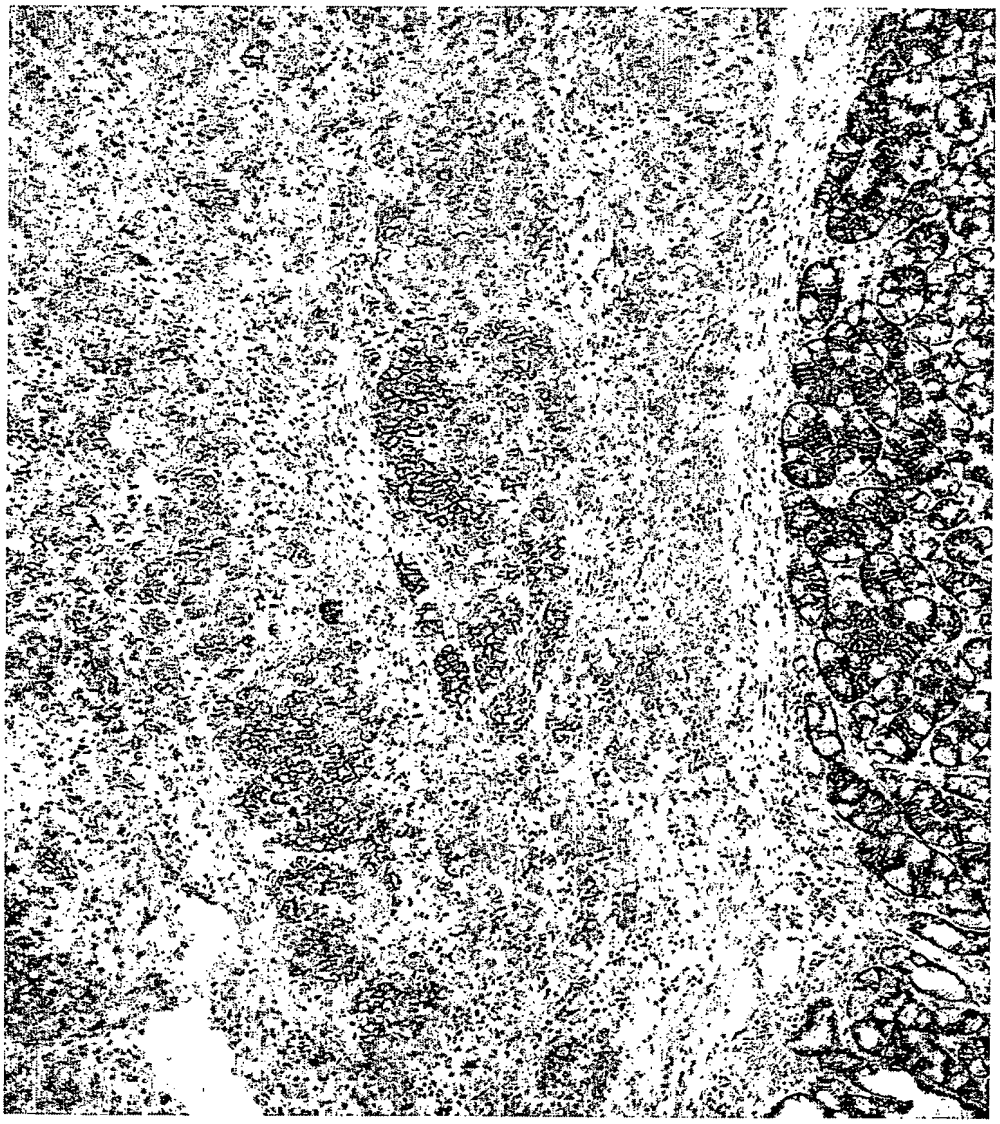


FIG. 17

FIG. 18

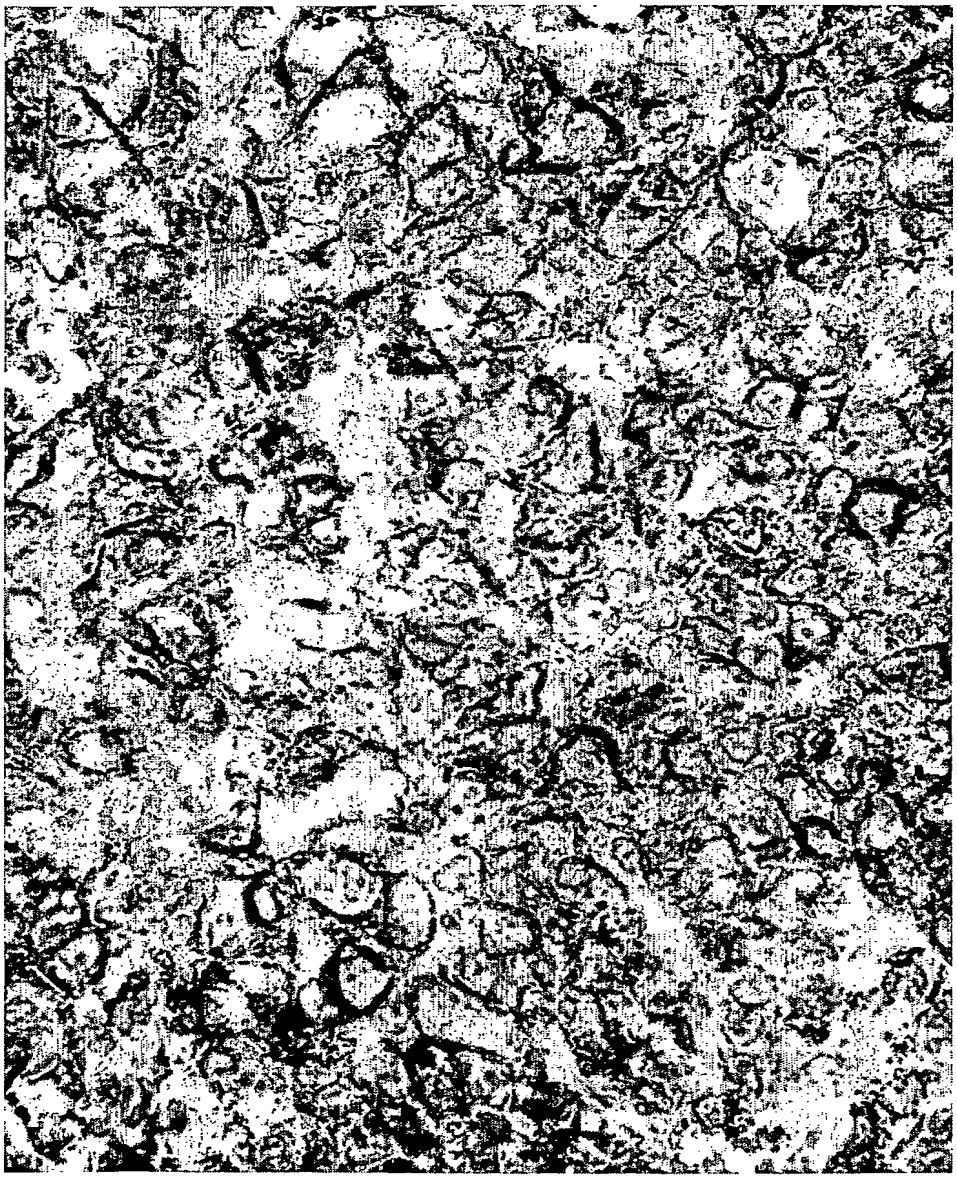


FIG. 19

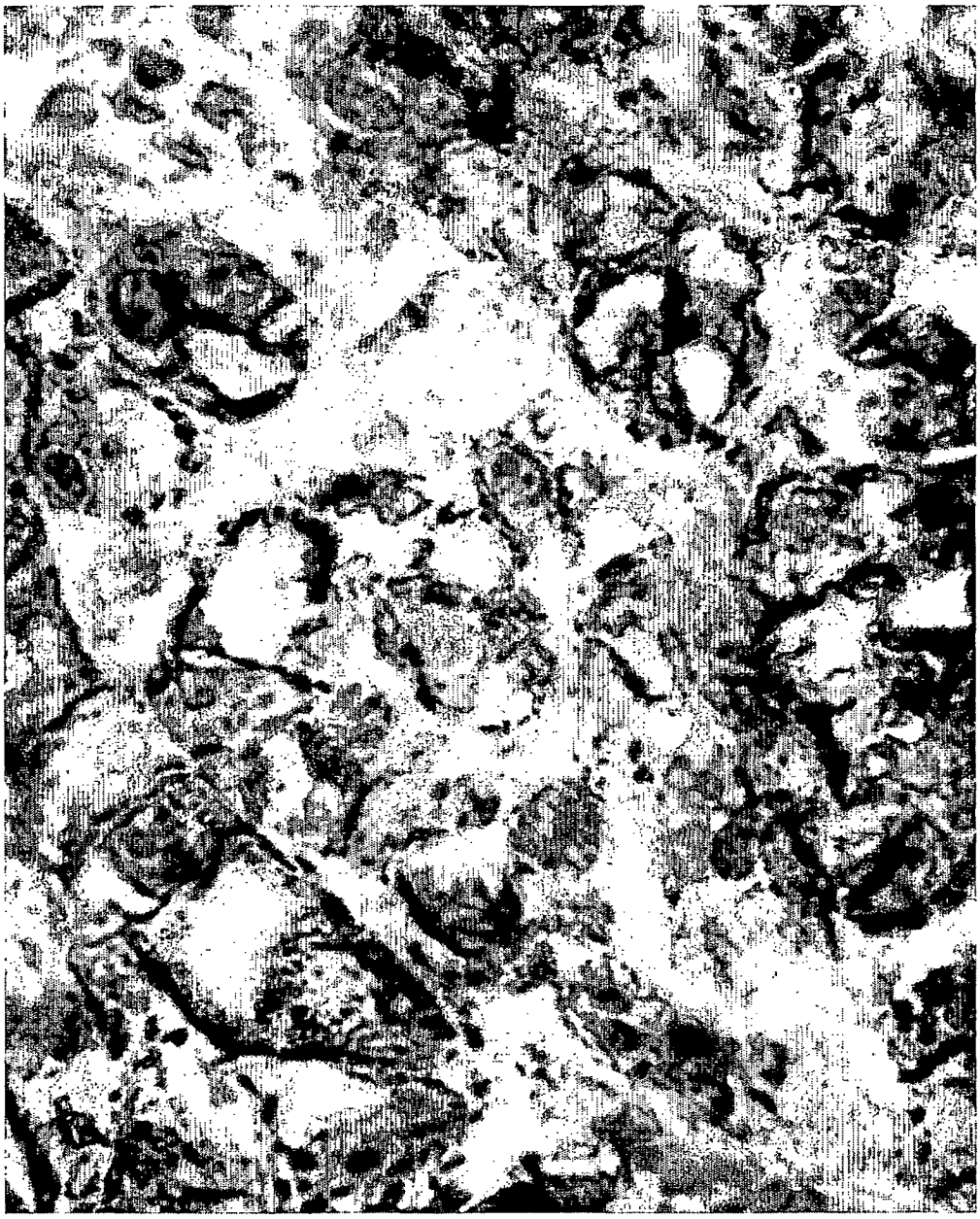


FIG. 20

TA-Bl-mur.A34 Light Chain Clone: 209-970

```
atgaggtgccttgttcagtttctggggctgcttgtgctctggatccct
M  R  C  L  V  Q  F  L  G  L  L  V  L  W  F  P
ggagccattggggatattgtgatgactcaggctgcaccctctgtccctgtcactcctgga
G  A  I  G  D  I  V  M  T  Q  A  A  P  S  V  P  V  T  P  G
gagtcagtatccatctcctgcaggtctagtacgagtctcctgcatagtaatggcaacact
E  S  V  S  I  S  C  R  S  S  T  S  L  L  H  S  N  G  N  T
tacttgtattggttcctgcagaggccaggccagtctcctcagctcctgatatatcggatg
Y  L  Y  W  F  L  Q  R  P  G  Q  S  P  Q  L  L  I  Y  R  M
tccaaccttgcctcaggagtcccagacaggttcagtggcagtgggtcaggaactgctttc
S  N  L  A  S  G  V  P  D  R  F  S  G  S  G  S  G  T  A  F
acactgagaatcagtagagtggaggctgaggatgtgggtatttattactgt[redacted]
T  L  R  I  S  R  V  E  A  E  D  V  G  I  Y  Y  C  M  Q  H
[redacted]ttcggaggggggaccaaactggaaataaaacgg
L  E  Y  P  F  T  F  G  G  G  T  K  L  E  I  K  R
```

(SEQ ID NO: 20)
(SEQ ID NO: 21)

TA-Bl-A34 Heavy Chain 4 Clone: 209-970

```
atgaactttgggttcagcttggttttccttgcccttattttaaaaggt
M  N  F  G  F  S  L  V  F  L  A  L  I  L  K  G
gtccagtgtgaggtggagctggtggagtctgggggaggcctagtgcagcctggagggtcc
V  Q  C  E  V  E  L  V  E  S  G  G  G  L  V  Q  P  G  G  S
ctgaaactctcctgtgcagcctctggattcaccttcagtactttggcatgtcttgggtt
L  K  L  S  C  A  A  S  G  F  T  F  S  T  F  G  M  S  W  V
cgccagactccagacaagaggctggagttggtcgcaaccattaatagtaatggtggtagg
R  Q  T  P  D  K  R  L  E  L  V  A  T  I  N  S  N  G  G  R
acctattatctagacagtgtgaagggccgattcaccatctccagagaaaatgccaagaac
T  Y  Y  L  D  S  V  K  G  R  F  T  I  S  R  E  N  A  K  N
accctgtacctgcaaatgagcagtctgaagtctgaggacacagccatgtattactgtgca
T  L  Y  L  Q  M  S  S  L  K  S  E  D  T  A  M  Y  Y  C  A
aga[redacted]ctggggccaagggactctg
R  D  G  G  L  L  R  D  S  A  W  F  A  Y  W  G  Q  G  T  L
gtcactgtctctgca   (SEQ ID NO: 22)
V  T  V  S  A    (SEQ ID NO: 23)
```

FIG. 21

TA-B1-mur.A34 Light Chain Clone: 209-564

atgaggtgccttgctcagcttctggggctgcttgtgctctggatccct
M R C L A Q L L C L L V L W I P
ggagccattggggatattgtgatgactcaggctgcaccctctgtacctgtcactcctgga
G A I G D I V M T Q A A P S V P V T P G
gagtcagtatccatctcctgcaggtctagtacgagtctcctgcatggtaatggcaacact
E S V S I S C R S S T S L L H G N G N T
tacttgtattggttcctgcagaggccaggccagtctcctcagctcctgatatatcggatg
Y L Y W F L Q R P G Q S P Q L L I Y R M
tccaaccttgcctcaggagtcccagacaggttcagtggcagtgggtcaggaactgctttc
S N L A S G V P D R F S G S G S G T A F
acactgagaatcagtagagtggaggctgaggatgtgggtatttattactgt[redacted]
T L R I S R V E A E D V G I Y Y C M Q H
[redacted]ttcggaggggggaccaagctggaaataaaacgg
L E Y P F T F G G G T K L E I K R
(SEQ ID NO: 24)
(SEQ ID NO: 25)

TA-B1-A34 Heavy Chain 4 Clone: 209-564

atggactttgggttcagcttggttttccttgcccttattttaaaaggt
M D F G F S L V F L A L I L K G
gtccagtgtgaggtggagctggtggagtctgggggaggcttagtgcagcctggagggtcc
V Q C E V E L V E S G G G L V Q P G G S
ctgaaactctcctgtgcagcctctggattcaccttcagtagttatggcatgtcttgggtt
L K L S C A A S G F T F S S Y G M S W V
cgccagactccagacaagaggctggagttggtcgcaaccattaatagtaatggtggtagg
R Q T P D K R L E L V A T I N S N G G R
acctattatctagacagtgtgaagggccgattcaccatctccagagacaatgccaagaac
T Y Y L D S V K G R F T I S R D N A K N
accctgtacctgcaaatgagcagtctgaagtctgaggacacagccatgtattactgtgca
T L Y L Q M S S L K S E D T A M Y Y C A
aga[redacted]tggggccaagggactctg
R D G G L L R D S A W F A Y W G Q G T L
gtcactgtctctgca
V T V S A
(SEQ ID NO: 26)
(SEQ ID NO: 27)

FIG. 22

TA-Bl-mur.A34 Light Chain Clone: 209-342

```
atgagggcccctgctcagattttggattcttgttgctctggttccca
M  R  A  P  A  Q  I  F  G  F  L  L  L  W  F  P
ggtgccagatgtgaaatccagatgacccagtctccatcctctatgtctgcatctctggga
G  A  R  C  E  I  Q  M  T  Q  S  P  S  S  M  S  A  S  L  G
gacagaataaccatcacttgccaggcaactcaagacattgttaaggaatttaaactggtat
D  R  I  T  I  T  C  Q  A  T  Q  D  I  V  K  N  L  N  W  Y
cagcagaaaccagggaaaccccccttcaatcctgatctattatgcaactgaactggcagaa
Q  Q  K  P  G  K  P  P  S  I  L  I  Y  Y  A  T  E  L  A  E
ggggtcccatcaaggttcagtggcagtgggtctgggtcagactattctctgacaatcagc
G  V  P  S  R  F  S  G  S  G  S  G  S  D  Y  S  L  T  I  S
aacctggagtctgaagattttgcagactattactgt[redacted]
N  L  E  S  E  D  F  A  D  Y  Y  C  L  Q  F  Y  D  F  P  L
[redacted]ttcggtgctgggaccaagctggagctgaaacgg  (SEQ ID NO:  28)
T  F  G  A  G  T  K  L  E  L  K  R    (SEQ ID NO:  29)
```

TA-Bl-mur.A34 Heavy Chain Clone:209-342

```
atgggatggagctatatcatcttctttctggtagcaacagctacaggt
M  G  W  S  Y  I  I  F  F  L  V  A  T  A  T  G
gtgcactcccaggtccagctgcagcagtctgggcctgagctggtgaggcctggggtctca
V  H  S  Q  V  Q  L  Q  Q  S  G  P  E  L  V  R  P  G  V  S
gtgaagatttcctgcaagggttccggctacacattcactgattatgctacgcactgggtg
V  K  I  S  C  K  G  S  G  Y  T  F  T  D  Y  A  T  H  W  V
aggcagagtcatgcaaagagtctagagtggattggagttattagtagttactctggtaat
R  Q  S  H  A  K  S  L  E  W  I  G  V  I  S  S  Y  S  G  N
acaaaagtacaaccagaactttaaggacaaggccacaatgactgtagacaaatcctccagc
T  K  Y  N  Q  N  F  K  D  K  A  T  M  T  V  D  K  S  S  S
acagcctatatggaacttgccagattgacatctgaggattctgccatgtattactgtgca
T  A  Y  M  E  L  A  R  L  T  S  E  D  S  A  M  Y  Y  C  A
aga[redacted]tggggtcaaggaacctcagtc
R  Y  D  Y  D  V  R  Y  Y  A  M  D  Y  W  G  Q  G  T  S  V
accgtctcctca  (SEQ ID NO:  30)
T  V  S  S    (SEQ ID NO:  31)
```

FIG. 23

TA-Bl-mur.A34 light chain clone 209-970

CDR1: SNGNTYLY	(SEQ ID NO: 32)
CDR2: RMSNLAS	(SEQ ID NO: 33)
CDR3: MQHLEYPFT	(SEQ ID NO: 34)

TA-Bl-A34 heavy chain clone 4 209-970

CDR1: TFGMS	(SEQ ID NO: 35)
CDR2: TINSNGGRTYYLDSVKG	(SEQ ID NO: 36)
CDR3: DGGLLRDSAWFAY	(SEQ ID NO: 37)

TA-Bl-mur.A34 light chain clone 209-564

CDR1: GNGNTYLY	(SEQ ID NO: 38)
CDR2: RMSNLAS	(SEQ ID NO: 39)
CDR3: MQHLEYPFT	(SEQ ID NO: 40)

TA-Bl-A34 heavy chain clone 4 209-564

CDR1: SYGMS	(SEQ ID NO: 41)
CDR2: TINSNGGRTYYLDSVKG	(SEQ ID NO: 42)
CDR3: DGGLLRDSAWFAY	(SEQ ID NO: 43)

TA-Bl-mur.A34 light chain clone 209-342

CDR1: QATQDIVKNLN	(SEQ ID NO: 44)
CDR2: YATELAE	(SEQ ID NO: 45)
CDR3: LQFYDFPLT	(SEQ ID NO: 46)

TA-Bl-mur.A34 heavy chain clone 209-342

CDR1: DYATH	(SEQ ID NO: 47)
CDR2: VISSYSGNT	(SEQ ID NO: 48)
CDR3: YDYDVRYYAMDY	(SEQ ID NO: 49)

FIG. 24

AGCGGGGCGATGCCCAGCAGATAAGCCAGGCAAACCTCGGTGTGATCGAAGAAGCCAATTTG
AGACTCAGCCTAGTCCAGGCAAGCTACTGGCACCTGCTGCTCTCAACTAACCTCCACACAAT
GGTGTTCGCATTTTGGAAGGTCTTTCTGATCCTAAGCTGCCTTGCAGGTCAGGTTAGTGTGG
TGCAAGTGACCATCCCAGACGGTTTCGTGAACGTGACTGTTGGATCTAATGTCACTCTCATC
TGCATCTACACCACCACTGTGGCCTCCCGAGAACAGCTTTCCATCCAGTGGTCTTTCTTCCA
TAAGAAGGAGATGGAGCCAATTTCTATTTACTTTTCTCAAGGTGGACAAGCTGTAGCCATCG
GGCAATTTAAAGATCGAATTACAGGGTCCAACGATCCAGGTAATGCATCTATCACTATCTCG
CATATGCAGCCAGCAGACAGTGGAATTTACATCTGCGATGTTAACAACCCCCCAGACTTTCT
CGGCCAAAACCAAGGCATCCTCAACGTCAGTGTGTTAGTGAAACCTTCTAAGCCCCTTTGTA
GCGTTCAAGGAAGACCAGAAACTGGCCACACTATTTCCCTTTCCTGTCTCTCTGCGCTTGGA
ACACCTTCCCCTGTGTACTACTGGCATAAACTTGAGGGAAGAGACATCGTGCCAGTGAAAGA
AAACTTCAACCCAACCACCGGGATTTTGGTCATTGGAAATCTGACAAATTTTGAACAAGGTT
ATTACCAGTGTACTGCCATCAACAGACTTGGCAATAGTTCCTGCGAAATCGATCTCACTTCT
TCACATCCAGAAGTTGGAATCATTGTTGGGGCCTTGATTGGTAGCCTGGTAGGTGCCGCCAT
CATCATCTCTGTTGTGTGCTTCGCAAGGAATAAGGCAAAAGCAAAGGCAAAAGAAAGAAATT
CTAAGACCATCGCGGAACTTGAGCCAATGACAAAGATAAACCCAAGGGGAGAAAGCGAAGCA
ATGCCAAGAGAAGACGCTACCCAACTAGAAGTAACTCTACCATCTTCCATTCATGAGACTGG
CCCTGATACCATCCAAGAACCAGACTATGAGCCAAAGCCTACTCAGGAGCCTGCCCCAGAGC
CTGCCCCAGGATCAGAGCCTATGGCAGTGCCTGACCTTGACATCGAGCTGGAGCTGGAGCCA
GAAACGCAGTCGGAATTGGAGCCAGAGCCAGAGCCAGAGCCAGAGTCAGAGCCTGGGGTTGT
AGTTGAGCCCTTAAGTGAAGATGAAAAGGGAGTGGTTAAGGCATAGGCTGGTGGCCTAAGTA
CAGCATTAATCATTAAGGAACCCATTACTGCCATTTGGAATTCAAATAACCTAACCAACCTC
CACCTCCTCCTTCCATTTTGACCAACCTTCTTCTAACAAGGTGCTCATTCCTACTATGAATC
CAGAATAAACACGCCAAGATAACAGCTAAATCAGCAAGGGTTCCTGTATTACCAATATAGAA
TACTAACAATTTTACTAACACGTAAGCATAACAAATGACAGGGCAAGTGATTTCTAACTTAG
TTGAGTTTTGCAACAGTACCTGTGTTGTTATTTCAGAAAATATTATTTCTCTCTTTTTAACT
ACTCTTTTTTTTTATTTTGGACAGAGTCTTGCTCCGTCGCGCAGGCTGTGATCGTAGTGGTG
CGATCTCGGCTCACTGCGGCCTCCGCTCCCTGGGTTCGGGCGATTCTCCTGCCTGGGCCTCC
TGAGTGGCTGGGACTGCAGGCACGTGCCGCCACGCCCGGCTAATTTTTTGTATTTTTGGTAG
AGATGGGGTTTCACGTTGTTGGCCAGGATGGTCTCCATCTCCTGACCTCATGATCCGCCCAC
CTTGGCCTCCCAAAATGCTGGGATTACAGGCATGAGCCACTGCGCCCGGCCTCTTTTTAGCT
ACTCTTATGTTCCACATGCACATATGACAAGGTGGCATTAATTAGATTCAATATTATTTCTA
GGAATAGTTCCTCATTCATTTTTATATTGACCACTAAGAAAATAATTCATCAGCATTATCTC
ATAGATTGGAAAATTTTCTCCAAATACAATAGAGGAGAATATGTAAAGGGTATACATTAATT
GGTACGTAGCATTTAAAATCAGGTCTTATAATTAATGCTTCATTCCTCATATTAGATTTCCC
AAGAAATCACCCTGGTATCCAATATCTGAGCATGGCAAATTTAAAAAATAACACAATTTCTT
GCCTGTGACCCTAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGGGTTCGA
GACCAGCCTGGCCGACATGGCGAAGCCCCTTCTCTGCTAGGAATGCAGAAATTGGCTGGGCG
TGGTGGTGCATGCCTGTAGTCCCGGCTACTTGGGAGGCTGAGGCAGGAGAGTCGCTTGAACC
CAGGGGGTGGAGGTTGCAGTGAGCCGAGATTGTGCCACTGCACTCCAACCTGGGTGACGGAG
TGAGATTCCATCTGAAAAACAAAAACAAAAACAGAAAACAAACAAACAAAAAACAAAAAATC
CCCACAACTTTGTCAAATAATGTACAGGCAAACACTTTCAAATATAATTTCCTTCAGTGAAT
ACAAAATGTTGATATCATAGGTGATGTACAATTTAGTTTTGAATGAGTTATTATGTTATCAC
TGTGTCTGATGTTATCTACTTTGAAAGGCAGTCCAGAAAAGTGTTCTAAGTGAACTCTTAAG
ATCTATTTTAGATAATTTCAACTAATTAAATAACCTGTTTTACTGCCTGTACATTCCACATT
AATAAAGCGATACCAATCTTATATGAATGCTAATATTACTAAAATGCACTGATATCACTTCT
TCTTCCACTGTTGAAAAGCTTTCTCATGATCATATTTCACCCACATCTCACCTTGAAGAAAC
TTACAGGTAGACTTACCTTTTCACTTGTGGAATTAATCATATTTAAATCTTACTTTAAGGCT
CAATAAATAATACTCATAATGTCCCAAAAAAAAAAAAAAAA (A34, SEQ ID
NO: 50)

FIG. 25

MVFAFWKVFLILSCLAGQVSVVQVTIPDGFVNVTVGSNVTLICIYTTTVASREQLSIQWSFF
HKKEMEPISIYFSQGGQAVAIGQFKDRITGSNDPGNASITISHMQPADSGIYICDVNNPPDF
LGQNQGILNVSVLVKPSKPLCSVQGRPETGHTISLSCLSALGTPSPVYYWHKLEGRDIVPVK
ENFNPTTGILVIGNLTNFEQGYYQCTAINRLGNSSCEIDLTSSHPEVGIIVGALIGSLVGAA
IIISVVCFARNKAKAKAKERNSKTIAELEPMTKINPRGESEAMPREDATQLEVTLPSSIHET
GPDTIQEPDYEPKPTQEPAPEPAPGSEPMAVPDLDIELELEPETQSELEPEPEPEPESEPGV
VVEPLSEDEKGVVKA (A34, SEQ ID NO: 1)

FIG. 26